

See short for case

001

5/3/06

TO: Ms. Patricia Booker, PCT DO/EO
FROM: Anne-Marie Corrigan, STIC

Per your request, please find copy of non-errored raw sequence listing for 10/516558.

Please contact me if you have any questions.

Thank you.

Total pages (including cover sheet): 9

*re-run***RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/516,558A
Source: PCF
Date Processed by STIC: 3/9/06

ENTERED

re-new

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

DATE: 05/03/2006
TIME: 15:20:20

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\05032006\J516558A.raw

3 <110> APPLICANT: Chano, Tokuhiro
 4 Okabe, Hidetoshi
 5 Ikegawa, Shiro
 7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene
 9 <130> FILE REFERENCE: 3190-070
 11 <140> CURRENT APPLICATION NUMBER: US 10/516,558A
 12 <141> CURRENT FILING DATE: 2004-11-30
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00682
 16 <151> PRIOR FILING DATE: 2003-01-30
 17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400
 18 <151> PRIOR FILING DATE: 2002-06-03
 20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978
 21 <151> PRIOR FILING DATE: 2002-07-24
 23 <160> NUMBER OF SEQ ID NOS: 132
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1594
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Unknown
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: human RB1CC1
 35 <400> SEQUENCE: 1
 37 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
 38 1 5 10 15
 41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
 42 20 25 30
 45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
 46 35 40 45
 49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
 50 50 55 60
 53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
 54 65 70 75 80
 57 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
 58 85 90 95
 61 Asp Met Glu Ile Lys Val Glu Ser Leu Met Met Pro Ala Val Phe
 62 100 105 110
 65 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
 66 115 120 125
 69 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
 70 130 135 140
 73 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
 74 145 150 155 160
 77 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser

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	165	170	175
78			His Leu
81 Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu			
82 180	185		190
85 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu			Glu Cys Leu
86 195	200		205
89 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro			
90 210	215	220	
93 Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu			240
94 225	230	235	
97 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr			
98 245	250	255	
101 Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala			
102 260	265	270	
105 Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln			
106 275	280	285	
109 Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe			
110 290	295	300	
113 Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp			320
114 305	310	315	
117 Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp			335
118 325	330	335	
121 Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala			
122 340	345	350	
125 Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg			
126 355	360	365	
128 Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn			
129 370	375	380	
132 Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala			400
133 385	390	395	
136 Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His			
137 405	410	415	
140 Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp			
141 420	425	430	
144 Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu			
145 435	440	445	
148 His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln			
149 450	455	460	
152 Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu			480
153 465	470	475	
156 Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr			
157 485	490	495	
160 Cys Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His			
161 500	505	510	
164 Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr			
165 515	520	525	
168 Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys			
169 530	535	540	
172 Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro			560
173 545	550	555	

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176 Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp	575
177 565 570	
180 Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu	590
181 580 585	
184 Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu	605
185 595 600	
188 His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser	620
189 610 615	
191 Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys	640
192 625 630 635	
195 Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met	655
196 645 650	
199 Glu Ser Thr Ala Gly Ile Thr Thr Thr Ser Pro Arg Thr Pro Pro	670
200 660 665	
203 Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu	685
204 675 680	
207 Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr	700
208 690 695	
211 Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp	720
212 705 710 715	
215 Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val	735
216 725 730	
219 Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser	750
220 740 745	
223 Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val	765
224 755 760	
227 Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly	780
228 770 775	
231 Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg	800
232 785 790 795	
235 Cys Arg val val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys	815
236 805 810	
239 Glu Asp Leu Cys His Phe Arg Thr Phe Val Gin Lys Glu Gln Cys Asp	830
240 820 825	
243 Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile	845
244 835 840	
247 Glu Lys val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln	860
248 850 855	
251 Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly	880
252 865 870 875	
254 Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys	895
255 885 890	
258 Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu	910
259 900 905	
262 Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn	925
263 915 920	
266 Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln	940
267 930 935	
270 Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu	

RAW SEQUENCE LISTING
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271	945	950	955	960
274	Asp Leu Lys Lys Leu His Val Glu Asn Asp	Glu Lys Leu Gln Leu Leu		
		970	975	
275	965			
278	Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys Glu Leu Glu			
	980	985	990	
279				
282	Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr			
	995	1000	1005	
283				
286	Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln			
	1010	1015	1020	
287	Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu			
	1025	1030	1035	
291				
294	Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu			
	1040	1045	1050	
295				
298	Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu			
	1055	1060	1065	
299				
302	Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala			
	1070	1075	1080	
303				
306	Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu			
	1085	1090	1095	
307				
310	Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp			
	1100	1105	1110	
311				
314	Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu			
	1115	1120	1125	
315				
317	Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg			
	1130	1135	1140	
318				
321	His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val			
	1145	1150	1155	
322				
325	Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys			
	1160	1165	1170	
326				
329	Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser			
	1175	1180	1185	
330				
333	Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu			
	1190	1195	1200	
334				
337	Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys			
	1205	1210	1215	
338				
341	Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys			
	1220	1225	1230	
342				
345	Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu			
	1235	1240	1245	
346				
349	Phe Lys Leu Glu Arg Glu Val Val Glu Lys Glu Leu Leu Glu Lys			
	1250	1255	1260	
350				
353	Val Lys His Leu Glu Asn Gln Ile Ala Lys Ser Pro Ala Ile Asp			
	1265	1270	1275	
354				
357	Ser Thr Arg Gly Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu			
	1280	1285	1290	
358				
361	Lys Leu Gln Glu Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu			
	1295	1300	1305	
362				
365	Gln Glu Lys Arg Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser			
	1310	1315	1320	

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369	Leu	Ile	Ala	Glu	Gln	Gln	Thr	Asn	Phe	Asn	Thr	Val	Leu	Thr	Arg
370		1325					1330					1335			
373	Glu	Lys	Met	Arg	Lys	Glu	Asn	Ile	Ile	Asn	Asp	Leu	Ser	Asp	Lys
374							1345					1350			
377	Leu	Lys	Ser	Thr	Met	Gln	Gln	Gln	Glu	Arg	Asp	Lys	Asp	Leu	Ile
378							1360					1365			
381	Glu	Ser	Leu	Ser	Glu	Asp	Arg	Ala	Arg	Leu	Leu	Glu	Glu	Lys	Lys
382							1375					1380			
385	Lys	Leu	Glu	Glu	Glu	Val	Ser	Lys	Leu	Arg	Ser	Ser	Ser	Phe	Val
386							1390					1395			
389	Pro	Ser	Pro	Tyr	Val	Ala	Thr	Ala	Pro	Glu	Leu	Tyr	Gly	Ala	Cys
390							1405					1410			
393	Ala	Pro	Glu	Leu	Pro	Gly	Glu	Ser	Asp	Arg	Ser	Ala	Vai	Glu	Thr
394							1420					1425			
397	Ala	Asp	Glu	Gly	Arg	Val	Asp	Ser	Ala	Met	Glu	Thr	Ser	Met	Met
398							1435					1440			
401	Ser	Val	Gln	Glu	Asn	Ile	His	Met	Leu	Ser	Glu	Glu	Lys	Gln	Arg
402							1450					1455			
405	Ile	Met	Ieu	Leu	Glu	Arg	Thr	Leu	Gln	Leu	Lys	Glu	Glu	Glu	Asn
406							1465					1470			
409	Lys	Arg	Leu	Asn	Gln	Arg	Leu	Met	Ser	Gln	Ser	Met	Ser	Ser	Val
410							1480					1485			
413	Ser	Ser	Arg	His	Ser	Glu	Lys	Ile	Ala	Ile	Arg	Asp	Phe	Gln	Val
414							1495					1500			
417	Gly	Asp	Leu	Val	Leu	Ile	Ile	Leu	Asp	Glu	Arg	His	Asp	Asn	Tyr
418							1510					1515			
421	Val	Leu	Phe	Thr	Val	Ser	Pro	Thr	Leu	Tyr	Phe	Leu	His	Ser	Glu
422							1525					1530			
425	Ser	Leu	Pro	Ala	Leu	Asp	Leu	Lys	Pro	Gly	Glu	Gly	Ala	Ser	Gly
426							1540					1545			
429	Ala	Ser	Arg	Arg	Pro	Trp	Val	Leu	Gly	Lys	Val	Met	Glu	Lys	Glu
430							1555					1560			
433	Tyr	Cys	Gln	Ala	Lys	Lys	Ala	Gln	Asn	Arg	Phe	Lys	Val	Pro	Leu
434							1570					1575			
437	Gly	Thr	Lys	Phe	Tyr	Arg	Val	Lys	Ala	Val	Ser	Trp	Asn	Lys	Lys
438							1585					1590			
441	Val														
446	<210>	SEQ ID NO:	2												
447	<211>	LENGTH:	1588												
448	<212>	TYPE:	PRT												
449	<213>	ORGANISM:	Unknown												
451	<220>	FEATURE:													
452	<223>	OTHER INFORMATION:	mouse Rbiccl												
454	<400>	SEQUENCE:	2												
456	Met	Lys	Leu	Tyr	Val	Phe	Leu	Val	Asn	Thr	Gly	Thr	Leu	Thr	Phe
457	1						5				10		15		
460	Asp	Thr	Glu	Leu	Thr	Val	Gln	Thr	Val	Ala	Asp	Leu	Lys	His	Ala
461												25	30		
464	Gln	Ser	Lys	Tyr	Lys	Ile	Ala	Ile	Gln	His	Gln	Val	Leu	Val	Asn

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/03/2006
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Invalid <213> Response!
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.
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Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
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Seq#:102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119
Seq#:120,121,122,123,124,125,126,127,128,129,130,131,132

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VERIFICATION SUMMARY
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